W187

Transposable Elements in the Robusta Coffee Genome (*Coffea canephora*)

Date: Sunday, January 12, 2014
Time: 4:40 PM
Room: Pacific Salon 4-5 (2nd Floor)

Stephanie Bocs , CIRAD, Montpellier, France
Alexis Dereeper , IRD, UMR RPB, Montpellier cedex 5, France
Thomas Gayraud , Institut de Recherche pour le Développement, Montpellier Cedex 5, France
Véronique Jamilloux , INRA - URGI, Versailles, France
Philippe Lashermes , Institut de Recherche pour le Développement, Montpellier cedex 5, France
***Romain Guyot** , Institut de Recherche pour le Développement, Montpellier cedex 5, France*

PDF file

Coffee is one of the most important international trade commodities and is ranked as the second most valuable primary commodity exported by southern countries. Two species are mainly used in commercial production: *Coffea arabica*, known as Arabica and *Coffea canephora*, a perennial diploid species known as Robusta. Recently, 54.4 million of Roche 454 sequences, 131,412 Sanger BAC-end sequences and 60X Illumina coverage of the 710 Mb genome of a *C. canephora* Double Haploid accession (DH200-94) were generated, assembled and anchored to a genetic map. The *C. canephora* genome sequence represents a formidable resource to understand the chromosome structure and the genome evolution. It is now well established that plant genomes are dynamic structures submitted to a wide range of modifications via the activity of Transposable Elements (TEs). Transposable elements are mobile sequences that share several key properties such as the ability to move from one chromosome location to another, to amplify their copy number within the host genome and to contribute to the chromosome structure, organization and evolution. Particularly, TEs play a major role in creating structural variation and genetic diversity in plant genomes. Here we present the identification and classification of TEs in the 568 Mb genomic sequences of the *C. canephora* using a combination of *ab initio,* similarity and structure search approaches. We used mainly the REPET package V.2.1-RC (Flutre et al., 2011) to identify, classify and annotate TE. We found that 49% of the genomic sequences are composed of TEs similarly to other sequenced plant genomes such as banana, papaya, castor bean and soybean. Class I LTR retrotransposons represent the vast majority of identified elements, accounting to 42% of the genome assembly. *Gypsy* elements clearly outnumbering *Copia* elements since *Ty3-Gypsy* family covers 24.1% of the genome. Interestingly active non-autonomous LTR retrotransposons elements were detected and classified into a new subgroup of non–autonomous elements containing a *capsid* domain but lacking the *polyprotein* region. Finally in an attempt to study conservation of LTR retrotransposons between coffee and reference plant genomes, we identified an outstanding conservation of several *Copia* groups across very distantly related plant species, suggesting that conservation of such elements or horizontal transfer events might be more frequent than recognized actually.

Back to: Coffee Genomics

<< Previous Abstract | Next Abstract >>